

SEQUENCE LISTING

<110> Novozymes Biotech, Inc.
 Connelly, Mariah
 Brody, Howard

<120> Methods For Producing Biological Substances In Enzyme-Deficient
 Mutants Of Aspergillus Niger

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<170> PatentIn version 3.2

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Ala Ser Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg
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175

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Tyr Ala Pro Leu Thr Lys Leu Gly Leu Leu Lys Leu Asp Arg Asn Pro
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Thr Ser Glu Ser Ser Ala Leu Asp Gln Ala Ala Gln Leu Arg Thr Arg						
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Leu Glu Lys Asp Gly Leu Val Val Thr Val Val Ala Glu Thr Leu Arg						
	595			600		605
Glu Gly Val Asp Gln Thr Tyr Ser Thr Ala Asp Ala Thr Gly Phe Asp						

610	615	620
Gly Val Val Val Val Asp Gly Ala Ala Ala Leu Phe Ala Ser Thr Ala		
625	630	635 640
Ser Ser Pro Leu Phe Pro Thr Gly Arg Pro Leu Gln Ile Phe Val Asp		
	645	650 655
Ala Tyr Arg Trp Gly Lys Pro Val Gly Val Cys Gly Gly Lys Ser Ser		
	660	665 670
Glu Val Leu Asp Ala Ala Asp Val Pro Glu Asp Gly Asp Gly Val Tyr		
	675	680 685
Ser Glu Glu Ser Val Asp Met Phe Val Glu Glu Phe Glu Lys Gly Leu		
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Ala Thr Phe Arg Phe Thr Asp Arg Phe Ala Leu Asp Ser		
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 <212> DNA
 <213> Aspergillus niger

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<210> 16
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 <213> Aspergillus niger

<400> 16
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<210> 17
 <211> 2443
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 <213> Aspergillus niger

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 <223> n=a,c,g or t

<400> 17

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aaaccccaaca gaaggcattt atgatggctg cgtggtggtc tctatttctg tacggccttc	240
aggtcgcggc acctgctttg gctgcaacgc ctgcggactg gcgatcgcaa tccatttatt	300
tccttctcac ggatcgattt gcaaggacgg atgggtcgac gactgcgact tgtaatactg	360
cggatcaggt gtgttggtac ctactagctt tcagaaagag gaatgtaaac tgacttgata	420
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 <211> 499
 <212> PRT
 <213> *Aspergillus niger*

<400> 18

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Tyr Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr
 35 40 45

Ala Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln
 50 55 60

Gly Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
 65 70 75 80

Ile Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr

85

90

95

Gly Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn
 100 105 110

Glu Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu
 115 120 125

His Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met
 130 135 140

Gly Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro
 145 150 155 160

Phe Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr
 165 170 175

Glu Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val
 180 185 190

Ser Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp
 195 200 205

Tyr Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu
 210 215 220

Arg Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr
 225 230 235 240

Asn Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp
 245 250 255

Pro Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn
 260 265 270

Tyr Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly
 275 280 285

Ser Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys
 290 295 300

Pro Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro

305		310		315		320
Arg Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala						
	325		330		335	
Ala Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln						
	340		345		350	
Glu Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr						
	355		360		365	
Trp Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala						
	370		375		380	
Ser Arg Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe						
	385		390		395	400
Val Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Pro						
	405		410		415	
Met Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn						
	420		425		430	
Lys Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly						
	435		440		445	
Tyr Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val						
	450		455		460	
Thr Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu						
	465		470		475	480
Pro Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys						
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Ser Ser Ser

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 <212> DNA
 <213> Aspergillus niger

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<210> 20
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<212> DNA
<213> Aspergillus niger

<400> 20
cactgtaatc gactgagcta c 21

<210> 21
<211> 2520
<212> DNA
<213> Aspergillus niger

<220>
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<223> n=a,c,g or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> n=a,c,g or t

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gccatgcttg gaggatagca accgacaaca tcacatcaag ctctcccttc tctgaacaat 180
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aaaaaaaaag aaggaaaagc agaagaaaaa taaaataaaa agaactctag tcctaaccat 540
cacatagttg gactatatcc agggaatggg cttcacagcc atctggatca cccccgttac 600
agcccagctg cccagacca ccgcatatgg agatgcctac catggctact ggcagcagga 660
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tgatggtttt agatactctc tgaacgaaaa ctacggcact gcagatgact tgaaggcgct 780
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agttcccaag actacttcca cccgttctgt ttcatcctaaa actatgaaga tcagactcag	1020
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gatgtgggtca agaataaatg gtacgactgg gtgggatcat tggatcga ctactccagt	1140
aagatatttc tccctcattc tacaacttgg ctgatcgatg atacttacga aatcagttga	1200
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<210> 22
 <211> 498
 <212> PRT
 <213> Aspergillus niger

<400> 22

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Ala Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile
 20 25 30

Tyr Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr
 35 40 45

Ala Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln
 50 55 60

Gly Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
 65 70 75 80

Ile Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr
 85 90 95

Gly Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn
 100 105 110

Glu Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu
 115 120 125

His Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met
 130 135 140

Gly Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro
 145 150 155 160

Phe Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr
 165 170 175

Glu Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val
 180 185 190

Ser Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp
 195 200 205

Tyr Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu
 210 215 220

Arg Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr
 225 230 235 240

Asn Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp
 245 250 255

Pro Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn
 260 265 270

Tyr Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly
 275 280 285

Ser Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys
 290 295 300

Pro Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro
 305 310 315 320

Arg Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala
 325 330 335

Ala Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln
 340 345 350

Glu Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr
 355 360 365

Trp Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala
 370 375 380

Ser Arg Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe
 385 390 395 400

Val Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Pro
 405 410 415

Met Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn
420 425 430

Lys Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly
435 440 445

Tyr Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val
450 455 460

Thr Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu
465 470 475 480

Pro Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys
485 490 495

Tyr Gly

<210> 23
<211> 3494
<212> DNA
<213> Aspergillus niger

<220>
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 gtcttgmtga ttca 3494

<210> 24
 <211> 341
 <212> PRT
 <213> Aspergillus niger

<400> 24

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Ala Arg Gln Glu Pro Val Val Asn Leu Asn Met Val Thr Gly Ala Ser		
35	40	45
Lys Leu Arg Lys Gln Leu Arg Glu Thr Asn Glu Leu Leu Val Cys Pro		
50	55	60
Gly Val Tyr Asp Gly Leu Ser Ala Arg Ile Ala Ile Asn Leu Gly Phe		
65	70	75 80
Lys Gly Met Tyr Met Thr Gly Ala Gly Thr Thr Ala Ser Arg Leu Gly		
	85	90 95
Met Ala Asp Leu Gly Leu Ala His Ile Tyr Asp Met Lys Thr Asn Ala		
	100	105 110
Glu Met Ile Ala Asn Leu Asp Pro Tyr Gly Pro Pro Leu Ile Ala Asp		
	115	120 125
Met Asp Thr Gly Tyr Gly Gly Pro Leu Met Val Ala Arg Ser Val Gln		
	130	135 140
Gln Tyr Ile Gln Ala Gly Val Ala Gly Phe His Ile Glu Asp Gln Ile		
145	150	155 160
Gln Asn Lys Arg Cys Gly His Leu Ala Gly Lys Arg Val Val Thr Met		
	165	170 175
Asp Glu Tyr Leu Thr Arg Ile Arg Ala Ala Lys Leu Thr Lys Asp Arg		
	180	185 190
Leu Arg Ser Asp Ile Val Leu Ile Ala Arg Thr Asp Ala Leu Gln Gln		
	195	200 205
His Gly Tyr Asp Glu Cys Ile Arg Arg Leu Lys Ala Ala Arg Asp Leu		
	210	215 220
Gly Ala Asp Val Gly Leu Leu Glu Gly Phe Thr Ser Lys Glu Met Ala		
225	230	235 240
Arg Arg Cys Val Gln Asp Leu Ala Pro Trp Pro Leu Leu Leu Asn Met		

245

250

255

Val Glu Asn Gly Ala Gly Pro Val Ile Ser Val Asp Glu Ala Arg Glu
 260 265 270

Met Gly Phe Arg Ile Met Ile Phe Ser Phe Ala Cys Ile Thr Pro Ala
 275 280 285

Tyr Met Gly Ile Thr Ala Ala Leu Glu Arg Leu Lys Lys Asp Gly Val
 290 295 300

Val Gly Leu Pro Glu Gly Met Gly Pro Lys Lys Leu Phe Glu Val Cys
 305 310 315 320

Gly Leu Met Asp Ser Val Arg Val Asp Thr Glu Ala Gly Gly Asp Gly
 325 330 335

Phe Ala Asn Gly Val
 340

<210> 25
 <211> 21
 <212> DNA
 <213> *Aspergillus niger*

<400> 25
 ctacgacatg aagaccaacg c 21

<210> 26
 <211> 21
 <212> DNA
 <213> *Aspergillus niger*

<400> 26
 gcaccgttct ccaccatggt g 21

<210> 27
 <211> 1389
 <212> DNA
 <213> *Candida antarctica*

<400> 27
 atgcgagtgt ccttgcgctc catcacgtcg ctgcttgccg cggaacggc ggctgtgctc 60

gcggctccgg cgcccgagac gctggaccga cgggcggcgc tgcccaaccc ctacgacgat 120

cccttctaca cgacgccatc caacatcggc acgtttgccca agggccagggt gatccaatct 180

cgcaaggtgc ccacggacat cggcaacgcc aacaacgctg cgtcgttcca gctgcagtac	240
cgcaccacca atacgcagaa cgaggcggtg gccgacgtgg ccaccgtgtg gatccccggcc	300
aagcccgctt cgccgccc aa gatcttttcg taccaggctt acgaggatgc cacggcgctc	360
gactgtgctc cgagctacag ctacctcact ggattggacc agccgaacaa ggtgacggcg	420
gtgctcgaca cgcccatcat catcggctgg gcgctgcagc agggctacta cgtcgtctcg	480
tccgaccacg aaggcttcaa agccgccttc atcgtctggc acgaagaggg catggctatc	540
ctcgacggca tccgcgcgct caagaactac cagaacctgc catccgacag caaggtcgct	600
cttgaggggt acagtggcgg agctcacgcc accgtgtggg cgacttcgct tgctgaatcg	660
tacgcgcccg agctcaacat tgtcgggtgtc tcgcacggcg gcacgcccgt gagcgccaag	720
gacaccttta cattcctcaa cggcgggacct ttcgccggct ttgccctggc ggggtgtttcg	780
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ggtcagcggc cgctcaagca gatccgcggc cgtggcttct gcctgccgca ggtgggtgtg	900
acctaccctt tcctcaacgt cttctcgctg gtcaacgaca cgaacctgct gaatgaggcg	960
ccgatcgcta gcatcctcaa gcaggagact gtgggtccagg ccgaagcgag ctacacggta	1020
tcggtgccca agttcccgcg cttcatctgg catgcgatcc ccgacgagat cgtgccgtac	1080
cagcctgcgg ctacctacgt caaggagcaa tgtgccaagg gcgccaacat caatttttcg	1140
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tttatcaagc aagccttcga cggcaccaca cccaagggtga tctgcggcac tcccatccct	1260
gctatcgctg gcatcaccac gccctcggcg gaccaagtgc tgggttcgga cctggccaac	1320
cagctgcgca gcctcgacgg caagcagagt gcgttcggca agccctttgg ccccatcaca	1380
ccaccttag	1389

<210> 28
 <211> 462
 <212> PRT
 <213> Candida antarctica

<220>
 <221> MISC_FEATURE
 <222> (1389) .. (1389)
 <223> X=Xaa

<400> 28

Met Arg Val Ser Leu Arg Ser Ile Thr Ser Leu Leu Ala Ala Ala Thr
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Ala Ala Val Leu Ala Ala Pro Ala Ala Glu Thr Leu Asp Arg Arg Ala
 20 25 30

Ala Leu Pro Asn Pro Tyr Asp Asp Pro Phe Tyr Thr Thr Pro Ser Asn
 35 40 45

Ile Gly Thr Phe Ala Lys Gly Gln Val Ile Gln Ser Arg Lys Val Pro
 50 55 60

Thr Asp Ile Gly Asn Ala Asn Asn Ala Ala Ser Phe Gln Leu Gln Tyr
 65 70 75 80

Arg Thr Thr Asn Thr Gln Asn Glu Ala Val Ala Asp Val Ala Thr Val
 85 90 95

Trp Ile Pro Ala Lys Pro Ala Ser Pro Pro Lys Ile Phe Ser Tyr Gln
 100 105 110

Val Tyr Glu Asp Ala Thr Ala Leu Asp Cys Ala Pro Ser Tyr Ser Tyr
 115 120 125

Leu Thr Gly Leu Asp Gln Pro Asn Lys Val Thr Ala Val Leu Asp Thr
 130 135 140

Pro Ile Ile Ile Gly Trp Ala Leu Gln Gln Gly Tyr Tyr Val Val Ser
 145 150 155 160

Ser Asp His Glu Gly Phe Lys Ala Ala Phe Ile Ala Gly Tyr Glu Glu
 165 170 175

Gly Met Ala Ile Leu Asp Gly Ile Arg Ala Leu Lys Asn Tyr Gln Asn
 180 185 190

Leu Pro Ser Asp Ser Lys Val Ala Leu Glu Gly Tyr Ser Gly Gly Ala
 195 200 205

His Ala Thr Val Trp Ala Thr Ser Leu Ala Glu Ser Tyr Ala Pro Glu
 210 215 220

Leu Asn Ile Val Gly Ala Ser His Gly Gly Thr Pro Val Ser Ala Lys
 225 230 235 240

Asp Thr Phe Thr Phe Leu Asn Gly Gly Pro Phe Ala Gly Phe Ala Leu
 245 250 255

Ala Gly Val Ser Gly Leu Ser Leu Ala His Pro Asp Met Glu Ser Phe
 260 265 270

Ile Glu Ala Arg Leu Asn Ala Lys Gly Gln Arg Thr Leu Lys Gln Ile
 275 280 285

Arg Gly Arg Gly Phe Cys Leu Pro Gln Val Val Leu Thr Tyr Pro Phe
 290 295 300

Leu Asn Val Phe Ser Leu Val Asn Asp Thr Asn Leu Leu Asn Glu Ala
 305 310 315 320

Pro Ile Ala Ser Ile Leu Lys Gln Glu Thr Val Val Gln Ala Glu Ala
 325 330 335

Ser Tyr Thr Val Ser Val Pro Lys Phe Pro Arg Phe Ile Trp His Ala
 340 345 350

Ile Pro Asp Glu Ile Val Pro Tyr Gln Pro Ala Ala Thr Tyr Val Lys
 355 360 365

Glu Gln Cys Ala Lys Gly Ala Asn Ile Asn Phe Ser Pro Tyr Pro Ile
 370 375 380

Ala Glu His Leu Thr Ala Glu Ile Phe Gly Leu Val Pro Ser Leu Trp
 385 390 395 400

Phe Ile Lys Gln Ala Phe Asp Gly Thr Thr Pro Lys Val Ile Cys Gly
 405 410 415

Thr Pro Ile Pro Ala Ile Ala Gly Ile Thr Thr Pro Ser Ala Asp Gln
 420 425 430

Val Leu Gly Ser Asp Leu Ala Asn Gln Leu Arg Ser Leu Asp Gly Lys
 435 440 445

Gln Ser Ala Phe Gly Lys Pro Phe Gly Pro Ile Thr Pro Pro
 450 455 460

<210> 29
 <211> 2794
 <212> DNA
 <213> *Scytalidium thermophilum*

<400> 29
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 ccacttgag catagcaggt ggatgacagc accggatacc tgacctccga tgttggcggg 180
 cccattcagg accagaccag cctcaaggca ggcattccggg gtccgaccct tcttgaggac 240
 tttatgttcc gccagaagat ccagcacttc gaccatgaac gggtaaggac ataatgtca 300
 cacgagcggc tgcgtgcccc cctatttccg agacattggg ctggctggct ggctgtgact 360
 gcttgagttt ggggacatac ggagtacctt actgacgcgc tgaaccactc caggttcccc 420
 aaagggcggg ccatgctcga ggcgctggag cacacgggac cttcacgagt tacgccgact 480
 ggagtaacat caccgcggcg tcctttctga acgccactgg aaagcagacg ccggtgtttg 540
 tccggttctc gaccgttgct gggctctcag ggagcgcaga cacggcgaga gacgttcattg 600
 gtttcgcgac gcggtttgta agttttgttg tgtttcattc gttccggtct gtagaggagg 660
 gttaggatat gagctaactg gtgtgtgtgt gtgaagtaca ctgatgaagg caactttgta 720
 cgtcccacgc atggctcctca attctcttat ctggcagcca tgtgggtcatt gtcgacgttg 780
 ctaacttgcg taggatatcg tcggaaacaa catcccggta ttcttcattc aagatgcaat 840
 ccagttccct gaccttatcc actcgggtcaa gccgcgtccc gacaacgaga ttccccaagc 900
 ggcgacggct catgattcag cttgggactt cttcagccag cagccaagca ccatggtaag 960
 caatggacca aggagccgca cctgggggtga catgccaggg agtacacaag gcgttccgat 1020
 gacctcgtg tgaccaaggc agtacaacac tccacggagg actcgaagag attcggcaat 1080
 atggaacaca gaactgacag gatggttagca cacgttggtc tgggccatgt ccggccacgg 1140
 aatccctcgc agctaccgcc atatggtacg ttgcctggc tgagatgacc gtgaatccat 1200
 ttctaacctc aagcccagga tggcttcggc gtccacacgt tccggtttgt caaagatgac 1260
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 tgggaagagg cgcaggttct ttctggcaag aatgccgact tccaccgtca ggacctctgg 1380

gatgctattg agtccgggaa cggaccagaa tgggatgtct gcgtccagat tgtcgatgag	1440
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tacgccccct tgacgaagct gggcctcttg aagctggatc gcaatccgac caactacttc	1560
gccgagacgg agcagggtcat gttccaaccc ggtcatatcg tccgcggcat cgacttcacg	1620
gaggatcccc tgctacaggg acgcctcttt tcgtaccttg acacgcagct gaaccggaat	1680
ggcggggcca actttgagca gctgcccac aacatgccgc gggtgccgat tcacaacaat	1740
aatcgcgacg gcgccggcca gatgttcac cacaggaaca agtatcctgt aagtgcctct	1800
tttgccctga tcgttggtgt gccggcttgc tgacagacgc agtacactcc caacaccctg	1860
aacagtgggt atccgcggca agccaaccaa aatgccggac gcggattctt cacagcgcct	1920
ggccgtaccg ccagcgggtgc cctcgtccgt gaggtgtcgc caacattcaa cgaccactgg	1980
tcgcagcccc gtctcttctt caactccctc actcccgtcg aacaacagtt cctcgtcaac	2040
gccatgcgct tcgaaatcag ccttgtgaag tcggaagaag tcaagaagaa cgtgctcacc	2100
cagctcaacc gcgtcagcca tgacgtggcc gtgcgcgtgg ccgccgctat cggcctcggc	2160
gcgcccagcg cggacgacac atactaccac aacaacaaga cggctggcgt ctcaatcggt	2220
ggaagcgggc cttgcctac catcaagact ctccgcgtcg gcatcctggc taccacgagc	2280
gagtcgagcg cgctggatca ggcggcccag ctccgcaccc gtctggaaaa ggacgggctt	2340
gtggtcacgg ttgtggctga aacgctgcgc gagggggtag accagacgta ctcgacggcg	2400
gatgccacgg gtttcgacgg cgttggtgtt gtggacgggg cggcggcgct gtttgccagc	2460
accgcgtcgt cgccgttggt cccgacgggc aggcggttgc agatctttgt ggacgcgtat	2520
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gatgttccgg aagacgggga cggggtgtat tcggaggagt cgggtggacat gtttgtggag	2640
gagtttgaga aggggttggc tactttcagg gtgagtcctg atgcctttgt ttgttgtgat	2700
gttattgttt tgttttgtct cggactttgt gaaagaatga cggactgacg tctttggtat	2760
ctagtttacc gatcggtttg ctctcgactc ttag	2794

<210> 30

<211> 717

<212> PRT

<213> *Scytalidium thermophilum*

<400> 30

Met Asn Arg Val Thr Asn Leu Leu Ala Trp Ala Gly Ala Ile Gly Leu
 1 5 10 15

Ala Gln Ala Thr Cys Pro Phe Ala Asp Pro Ala Ala Leu Tyr Ser Arg
 20 25 30

Gln Asp Thr Thr Ser Gly Gln Ser Pro Leu Ala Ala Tyr Glu Val Asp
 35 40 45

Asp Ser Thr Gly Tyr Leu Thr Ser Asp Val Gly Gly Pro Ile Gln Asp
 50 55 60

Gln Thr Ser Leu Lys Ala Gly Ile Arg Gly Pro Thr Leu Leu Glu Asp
 65 70 75 80

Phe Met Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro
 85 90 95

Glu Arg Ala Val His Ala Arg Gly Ala Gly Ala His Gly Thr Phe Thr
 100 105 110

Ser Tyr Ala Asp Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala
 115 120 125

Thr Gly Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly
 130 135 140

Ser Arg Gly Ser Ala Asp Thr Ala Arg Asp Val His Gly Phe Ala Thr
 145 150 155 160

Arg Phe Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Ile
 165 170 175

Pro Val Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His
 180 185 190

Ser Val Lys Pro Arg Pro Asp Asn Glu Ile Pro Gln Ala Ala Thr Ala
 195 200 205

His Asp Ser Ala Trp Asp Phe Phe Ser Gln Gln Pro Ser Thr Met His
 210 215 220

Thr Leu Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Tyr Arg
 225 230 235 240

His Met Asp Gly Phe Gly Val His Thr Phe Arg Phe Val Lys Asp Asp
 245 250 255

Gly Ser Ser Lys Leu Ile Lys Trp His Phe Lys Ser Arg Gln Gly Lys
 260 265 270

Ala Ser Leu Val Trp Glu Glu Ala Gln Val Leu Ser Gly Lys Asn Ala
 275 280 285

Asp Phe His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Asn Gly
 290 295 300

Pro Glu Trp Asp Val Cys Val Gln Ile Val Asp Glu Ser Gln Ala Gln
 305 310 315 320

Ala Phe Gly Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu
 325 330 335

Tyr Ala Pro Leu Thr Lys Leu Gly Leu Leu Lys Leu Asp Arg Asn Pro
 340 345 350

Thr Asn Tyr Phe Ala Glu Thr Glu Gln Val Met Phe Gln Pro Gly His
 355 360 365

Ile Val Arg Gly Ile Asp Phe Thr Glu Asp Pro Leu Leu Gln Gly Arg
 370 375 380

Leu Phe Ser Tyr Leu Asp Thr Gln Leu Asn Arg Asn Gly Gly Pro Asn
 385 390 395 400

Phe Glu Gln Leu Pro Ile Asn Met Pro Arg Val Pro Ile His Asn Asn
 405 410 415

Asn Arg Asp Gly Ala Gly Gln Met Phe Ile His Arg Asn Lys Tyr Pro
 420 425 430

Tyr Thr Pro Asn Thr Leu Asn Ser Gly Tyr Pro Arg Gln Ala Asn Gln
 435 440 445

Asn Ala Gly Arg Gly Phe Phe Thr Ala Pro Gly Arg Thr Ala Ser Gly
 450 455 460

Ala Leu Val Arg Glu Val Ser Pro Thr Phe Asn Asp His Trp Ser Gln
 465 470 475 480

Pro Arg Leu Phe Phe Asn Ser Leu Thr Pro Val Glu Gln Gln Phe Leu
 485 490 495

Val Asn Ala Met Arg Phe Glu Ile Ser Leu Val Lys Ser Glu Glu Val
 500 505 510

Lys Lys Asn Val Leu Thr Gln Leu Asn Arg Val Ser His Asp Val Ala
 515 520 525

Val Arg Val Ala Ala Ala Ile Gly Leu Gly Ala Pro Asp Ala Asp Asp
 530 535 540

Thr Tyr Tyr His Asn Asn Lys Thr Ala Gly Val Ser Ile Val Gly Ser
 545 550 555 560

Gly Pro Leu Pro Thr Ile Lys Thr Leu Arg Val Gly Ile Leu Ala Thr
 565 570 575

Thr Ser Glu Ser Ser Ala Leu Asp Gln Ala Ala Gln Leu Arg Thr Arg
 580 585 590

Leu Glu Lys Asp Gly Leu Val Val Thr Val Val Ala Glu Thr Leu Arg
 595 600 605

Glu Gly Val Asp Gln Thr Tyr Ser Thr Ala Asp Ala Thr Gly Phe Asp
 610 615 620

Gly Val Val Val Val Asp Gly Ala Ala Ala Leu Phe Ala Ser Thr Ala
 625 630 635 640

Ser Ser Pro Leu Phe Pro Thr Gly Arg Pro Leu Gln Ile Phe Val Asp
 645 650 655

Ala Tyr Arg Trp Gly Lys Pro Val Gly Val Cys Gly Gly Lys Ser Ser
 660 665 670

Glu Val Leu Asp Ala Ala Asp Val Pro Glu Asp Gly Asp Gly Val Tyr
675 680 685

Ser Glu Glu Ser Val Asp Met Phe Val Glu Glu Phe Glu Lys Gly Leu
690 695 700

Ala Thr Phe Arg Phe Thr Asp Arg Phe Ala Leu Asp Ser
705 710 715